Amendments to the Specification

Replace all prior versions of the Sequence Listing with the substitute Sequence Listing printout filed herewith. Also filed herewith is a machine-readable version of the accompanying substitute Sequence Listing printout, the content of which is identical to the substitute Sequence Listing printout. It is believed that no new matter is presented by this substitution.

Amend paragraph 0009 of the Specification as follows:

[0009] In other research the oligomerisation domain of cartilage oligomeric matrix protein (COMP) has been used as a tool for multimerising several proteins in the past. COMP has been described and characterised by Efimov and colleagues (see e.g. Proteins: Structure, Function, and Genetics 24:259-262 (1996)). COMP is a pentameric glycoprotein of the thrombospondin family. Self-assembly of the protein to form pentamers is achieved through the formation of a five-stranded helical bundle that involves 64 N-terminal amino acid residues of the protein. The amino acid sequence of the oligomerisation domain has been disclosed by Efimov *et al.*, FEBS Letters 341:54-58 (1994), which for rat COMP reads as follows: QGQIPLGGDLAPQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDA CGMQPARTPGLSV [SEQ ID NO: 22], corresponding to amino acid residues ~~21~~20-83 of rat COMP.

Amend paragraph 0098 of the Specification as follows:

[0098] The whole region is synthesized using the overlapping complementary oligonucleotides (BMC#3, BMC#4, BMC#5, BMC#6, BMC#7 and BMC#8) [SEQ ID NOS: 8, 9, 10, 11, 12 and 13] in a 'PCR assembly' reaction. Oligonucleotide sequences are detailed in Appendix I and are synthesised and purified ('PAGE-pure') by Sigma-Genosys. The primers (4.8 pmoles) are phosphorylated with T4 kinase (10 U, Gibco) for 1 hour at 37°C, in forward reaction buffer (as supplied), supplemented with 1 mM ATP. The reaction is terminated by heating to 80°C for 15 min and then allowed to cool to room temperature, which enabled oligonucleotide annealling. The annealed oligonucleotides are ligated together using T4 DNA ligase as in Paragraphs 0088-0096 above, and ~10 ng used in a PCR to 'fill in' the ends of the sequences and to amplify the synthetic gene. The PCR reaction is essentially as described in Paragraphs 0088-0096 above, except BMC#3 [SEQ ID NO: 8] (15 µM) and BMC#8 [SEQ ID NO: 13] (15 µM) are used as the forward and reverse primers in the following thermal cycling conditions: Step 1: 95 °C, 4 min; Step 2: 95°C, 1 min; Step 3: 70°C, 1 min; Step 4: 72°C, 2 min; Step 5: cycle to Step 2, 15x; Step 6: 72°C, 10 min. A PCR product of the correct size is gel purified as detailed previously (Paragraphs 0088-0096

above). ~~This PCR product codes for a protein sequence which comprises the sequence QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT FLKNTVMECD ACGMQQSVRT GLPSVRP [SEQ ID NO: 24], which is identical to amino acids 21-87 of SEQ ID NO: 23.~~

Amend the table at Appendix II on page 41 of the Specification as follows:

Appendix II: Table of Disclosed Amino Acid Sequences

Sequence ID No.	**Amino Acid Sequence**
1	GLCTLVAML
6	SLNDIFEAQKIEWHE
7	PQPQPKPQPKPEPET
16	GS(GGGGS)$_4$GGK
17	G(GGGGS)$_4$GGK
22	QGQIPLGGDLAPQMLRELQETNAALQDVRELLR QQVKEITFLKNTVMECDACGMQPARTPGLSV
23	MVPDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ EDVDRDGIGD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWGDACDN CRSQKNDDQK DTDQDGRGDA CDDDIDGDRI RNQADNCPRV PNSDQKDSDG DGIGDACDNC PQKSNPDQAD VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPDS RDNCRLVPNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI FGYQDSSSFY VVMWKQMEQT YWQANPFRAV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT ESQVRLLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA
~~24~~	~~QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT FLKNTVMECD ACGMQQSVRT GLPSVRP~~